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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/905,657

DATE: 07/27/2001

TIME: 11:16:17

Input Set : A:\engl Sequenzprotokoll Le A 34 730.txt

Output Set: N:\CRF3\07272001\I905657.raw

3 <110> APPLICANT: BAYER AG
 5 <120> TITLE OF INVENTION: Use of VLCFAE for identifying herbicidally
 6 active compounds
 8 <130> FILE REFERENCE: Le A 34 730
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/905,657
 C--> 11 <141> CURRENT FILING DATE: 2001-07-13
 13 <160> NUMBER OF SEQ ID NOS: 2
 15 <170> SOFTWARE: PatentIn Ver. 2.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2782
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Arabidopsis thaliana
 22 <220> FEATURE:
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 39 cttcatcaac ctatagatct cactcacata atcaacctac aaaacaaaaa caaga atg 178
 40 Met
 41 1
 43 ggt aga tcc aac gag caa gat ctg ctc tct acc gag atc gtt aat cgt 226
 44 Gly Arg Ser Asn Glu Gln Asp Leu Leu Ser Thr Glu Ile Val Asn Arg
 45 5 10 15
 47 ggg atc gaa cca tcc ggt cct aac gcc ggc tca cca acg ttc tcg gtt 274
 48 Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe Ser Val
 49 20 25 30
 51 agg gtc agg aga cgt ttg cct gat ttt ctt cag tcg gtg aac ttg aag 322
 52 Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn Leu Lys
 53 35 40 45
 55 tac gtg aaa ctt ggt tac cac tac ctc ata aac cat gcg gtt tat ttg 370
 56 Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val Tyr Leu
 57 50 55 60 65
 59 gcg acc ata ccg gtt ctt gtg ctg gtt ttt agt gct gag gtt ggg agt 418
 60 Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val Gly Ser
 61 70 75 80
 63 tta agc aga gaa gag att tgg aag aag ctt tgg gac tat gat ctt gca 466
 64 Leu Ser Arg Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp Leu Ala
 65 85 90 95
 67 act gtt atc gga ttc ttc ggt gtc ttt gtt tta acc gct tgt gtc tac 514
 68 Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Ala Cys Val Tyr

ENTERED

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71 ttc atg tct cgt cct cgc tct gtt tat ctt att gat ttc gct tgt tac 562
72 Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala Cys Tyr
73          115          120          125
75 aag ccc tcc gat gaa cac aag gtacgtccca acctttccat agaggaaata 613
76 Lys Pro Ser Asp Glu His Lys
77 130          135
79 gtctaaatta cttttaccca aaaaaaaaaa aaaaaaaaaa atctaaatta agtatactta 673
81 agaaattata attagatttg tcaaaaaata ataattataa ttagatggat tagttgttta 733
83 tagggctgcc taaataaaat aaaattttgc ctttgcatgt gttacgtag taattatttt 793
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91 aaacaatcca aatttacgac ctataatcaa aggagattga taggaaccgg actgataatt 1033
93 aaatgaagct gaatcaaac aaacaaaagt tcatttaatt cgggttctct cgggtttaat 1093
95 ctctttttgc attggattgg ttttag gtg aca aaa gaa gag ttc ata gaa cta 1145
96          Val Thr Lys Glu Glu Phe Ile Glu Leu
97          140          145
99 gcg aga aaa tca ggg aag ttc gac gaa gag aca ctc ggt ttc aag aag 1193
100 Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Thr Leu Gly Phe Lys Lys
101          150          155          160
103 agg atc tta caa gcc tca ggc ata ggc gac gag aca tac gtc cca aga 1241
104 Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val Pro Arg
105          165          170          175
107 tcc atc tct tca tca gaa aac ata aca acg atg aaa gaa ggt cgt gaa 1289
108 Ser Ile Ser Ser Ser Glu Asn Ile Thr Thr Met Lys Glu Gly Arg Glu
109          180          185          190
111 gaa gcc tct aca gtg atc ttt gga gca cta gac gaa ctc ttc gag aag 1337
112 Glu Ala Ser Thr Val Ile Phe Gly Ala Leu Asp Glu Leu Phe Glu Lys
113          195          200          205
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117 210          215          220          225
119 att ttc aac ccg aca ccg tcg ttg tcc gca atg gtg ata aac cat tac 1433
120 Ile Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Ile Asn His Tyr
121          230          235          240
123 aag atg aga ggg aac ata ctt agt tac aac ctt gga ggg atg gga tgt 1481
124 Lys Met Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly Cys
125          245          250          255
127 tcg gct gga atc ata gct att gat ctt gct cgt gac atg ctt cag tct 1529
128 Ser Ala Gly Ile Ile Ala Ile Asp Leu Ala Arg Asp Met Leu Gln Ser
129          260          265          270
131 aac cct aat agt tat gct gtt gtt gtg agt act gag atg gtt ggg tat 1577
132 Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val Gly Tyr
133          275          280          285
135 aat tgg tac gtg gga agt gac aag tca atg gtt ata cct aat tgt ttc 1625
136 Asn Trp Tyr Val Gly Ser Asp Lys Ser Met Val Ile Pro Asn Cys Phe
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139 ttt agg atg ggt tgt tct gcc gtt atg ctc tct aac cgt cgt cgt gac 1673

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145          325          330          335
147 gct gct gac gac cgt agc ttc agg ttccattcat ttgggtatta attcggttta 1775
148 Ala Ala Asp Asp Arg Ser Phe Arg
149          340          345
151 caatctcttg accgacctag taactaattt tgtgtggttt ttagg agt gtg tac cag 1832
152          Ser Val Tyr Gln
154 gaa gaa gat gaa caa gga ttc aag ggg ttg aag ata agt aga gac tta 1880
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156 350          355          360          365
158 atg gaa gtt gga ggt gaa gct ctc aag aca aac atc act acc tta ggt 1928
159 Met Glu Val Gly Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly
160          370          375          380
162 cct ctt gtc cta cct ttc tcc gag cag ctt ctc ttc ttt gct gct ttg 1976
163 Pro Leu Val Leu Pro Phe Ser Glu Gln Leu Leu Phe Phe Ala Ala Leu
164          385          390          395
166 ctc cgc cga aca ttc tca cct gct gcc aaa acg tcc aca acc act tcc 2024
167 Leu Arg Arg Thr Phe Ser Pro Ala Ala Lys Thr Ser Thr Thr Ser
168          400          405          410
170 ttc tct act tcc gcc acc gca aaa acc aat gga atc aag tct tcc tct 2072
171 Phe Ser Thr Ser Ala Thr Ala Lys Thr Asn Gly Ile Lys Ser Ser Ser
172          415          420          425
174 tcc gat ctg tcc aag cca tac atc ccg gac tac aag ctc gcc ttc gag 2120
175 Ser Asp Leu Ser Lys Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu
176 430          435          440          445
178 cat ttt tgc ttc cac gcg gca agc aaa gta gtg ctt gaa gag ctt caa 2168
179 His Phe Cys Phe His Ala Ala Ser Lys Val Val Leu Glu Glu Leu Gln
180          450          455          460
182 aag aat cta ggc ttg agt gaa gag aat atg gag gct tct agg atg aca 2216
183 Lys Asn Leu Gly Leu Ser Glu Glu Asn Met Glu Ala Ser Arg Met Thr
184          465          470          475
186 ctt cac agg ttt gga aac act tct agc agt gga atc tgg tat gag ttg 2264
187 Leu His Arg Phe Gly Asn Thr Ser Ser Ser Gly Ile Trp Tyr Glu Leu
188          480          485          490
190 gct tac atg gag gcc aag gaa agt gtt cgt aga ggc gat agg gtt tgg 2312
191 Ala Tyr Met Glu Ala Lys Glu Ser Val Arg Arg Gly Asp Arg Val Trp
192          495          500          505
194 cag atc gct ttc ggt tct ggt ttt aag tgt aac agt gtg gtg tgg aag 2360
195 Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys
196 510          515          520          525
198 gca atg agg aag gtg aag aag cca acc agg aac aat cct tgg gtg gat 2408
199 Ala Met Arg Lys Val Lys Lys Pro Thr Arg Asn Asn Pro Trp Val Asp
200          530          535          540
202 tgc atc aac cgt tac cct gtg cct ctc taa attatcattc ttctaaatta 2458
203 Cys Ile Asn Arg Tyr Pro Val Pro Leu
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212 gattaaagaa aaaaactctt ctttagtttg atagaacaga tggtcattgt aatttcttta 2698
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232 35 40 45
234 Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val Tyr
235 50 55 60
237 Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val Gly
238 65 70 75 80
240 Ser Leu Ser Arg Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp Leu
241 85 90 95
243 Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Ala Cys Val
244 100 105 110
246 Tyr Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala Cys
247 115 120 125
249 Tyr Lys Pro Ser Asp Glu His Lys Val Thr Lys Glu Glu Phe Ile Glu
250 130 135 140
252 Leu Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Thr Leu Gly Phe Lys
253 145 150 155 160
255 Lys Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val Pro
256 165 170 175
258 Arg Ser Ile Ser Ser Ser Glu Asn Ile Thr Thr Met Lys Glu Gly Arg
259 180 185 190
261 Glu Glu Ala Ser Thr Val Ile Phe Gly Ala Leu Asp Glu Leu Phe Glu
262 195 200 205
264 Lys Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val Asn Cys
265 210 215 220
267 Ser Ile Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Ile Asn His
268 225 230 235 240
270 Tyr Lys Met Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly
271 245 250 255
273 Cys Ser Ala Gly Ile Ile Ala Ile Asp Leu Ala Arg Asp Met Leu Gln
274 260 265 270
276 Ser Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val Gly
277 275 280 285
279 Tyr Asn Trp Tyr Val Gly Ser Asp Lys Ser Met Val Ile Pro Asn Cys
280 290 295 300

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282 Phe Phe Arg Met Gly Cys Ser Ala Val Met Leu Ser Asn Arg Arg Arg
 283 305 310 315 320
 285 Asp Phe Arg His Ala Lys Tyr Arg Leu Glu His Ile Val Arg Thr His
 286 325 330 335
 288 Lys Ala Ala Asp Asp Arg Ser Phe Arg Ser Val Tyr Gln Glu Glu Asp
 289 340 345 350
 291 Glu Gln Gly Phe Lys Gly Leu Lys Ile Ser Arg Asp Leu Met Glu Val
 292 355 360 365
 294 Gly Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val
 295 370 375 380
 297 Leu Pro Phe Ser Glu Gln Leu Leu Phe Phe Ala Ala Leu Leu Arg Arg
 298 385 390 395 400
 300 Thr Phe Ser Pro Ala Ala Lys Thr Ser Thr Thr Thr Ser Phe Ser Thr
 301 405 410 415
 303 Ser Ala Thr Ala Lys Thr Asn Gly Ile Lys Ser Ser Ser Ser Asp Leu
 304 420 425 430
 306 Ser Lys Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu His Phe Cys
 307 435 440 445
 309 Phe His Ala Ala Ser Lys Val Val Leu Glu Glu Leu Gln Lys Asn Leu
 310 450 455 460
 312 Gly Leu Ser Glu Glu Asn Met Glu Ala Ser Arg Met Thr Leu His Arg
 313 465 470 475 480
 315 Phe Gly Asn Thr Ser Ser Ser Gly Ile Trp Tyr Glu Leu Ala Tyr Met
 316 485 490 495
 318 Glu Ala Lys Glu Ser Val Arg Arg Gly Asp Arg Val Trp Gln Ile Ala
 319 500 505 510
 321 Phe Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys Ala Met Arg
 322 515 520 525
 324 Lys Val Lys Lys Pro Thr Arg Asn Asn Pro Trp Val Asp Cys Ile Asn
 325 530 535 540
 327 Arg Tyr Pro Val Pro Leu
 328 545 550

VERIFICATION SUMMARY

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Input Set : A:\engl Sequenzprotokoll Le A 34 730.txt

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date